IN THE SPECIFICATION:

Please replace the first paragraph on page 1 with the following amended paragraph:

This application claims priority to U.S. Provisional Application Serial No. 60/276,179 filed on March 15, 2001, U.S. Provisional Application Serial No. 60/307,233 filed on July 23, 2001, and U.S. Provisional Application Serial No. 60/343,818 filed on October 25, 2001, all of which are incorporated herein by reference in their entirety.

Please replace the last paragraph on page 17 with the following amended paragraph:

For the purpose of comparing two different nucleic acid or polypeptide sequences, one sequence (test sequence) may be described to be a specific "percent identical to" another sequence (reference sequence) in the present disclosure. In this respect, when the length of the test sequence is less than 90% of the length of the reference sequence, the percentage identity is determined by the algorithm of Myers and Miller, *Bull. Math. Biol.*, 51:5-37 (1989) and Myers and Miller, *Comput. Appl. Biosci.*, 4(1):11-7 (1988). Specifically, the identity is determined by the ALIGN program, which is available at ~~http://www2.igh.cnrs.fr maintained by IGH~~, the Institut de Genetique Humaine website, Montpellier, FRANCE. The default parameters can be used.

Please replace the first paragraph on page 18 with the following amended paragraph:

Where the length of the test sequence is at least 90% of the length of the reference sequence, the percentage identity is determined by the algorithm of Karlin and Altschul, *Proc. Natl. Acad. Sci. USA*, 90:5873-77 (1993), which is incorporated into various BLAST programs. Specifically, the percentage identity is determined by the "BLAST 2 Sequences" tool, which is available at ~~http://www.ncbi.nlm.nih.gov/gorf/bl2.html~~ the NCBI National Center for Biotechnology Information website. *See* Tatusova and Madden, *FEMS Microbiol. Lett.*, 174(2):247-50 (1999). For pairwise DNA-DNA comparison, the BLASTN 2.1.2 program is used with default parameters (Match: 1;

Mismatch: -2; Open gap: 5 penalties; extension gap: 2 penalties; gap x_dropoff: 50; expect: 10; and word size: 11, with filter). For pairwise protein-protein sequence comparison, the BLASTP 2.1.2 program is employed using default parameters (Matrix: BLOSUM62; gap open: 11; gap extension: 1; x_dropoff: 15; expect: 10.0; and wordsize: 3, with filter).

Please replace the table on page 21 with the following amended table:

Table 1: Binding Regions of Survivin and Its Interacting Partners

Bait Protein			Prey Proteins			
Name and GenBank Accession No.	Amino Acid Coordinates		Names	GenBank Accession Nos.	Amino Acid Coordinates	
	Start	Stop			Start	Stop
Survivin (BIRC5) Accession Number U75285	89	~~143~~ 142	Cytoplasmic dynein light chain 1 (HDLC1)	U32944	1	90
	3	99	Cytoplasmic dynein light chain 1 (HDLC1)	U32944	-20	89
	47	~~143~~ 142	Cytoplasmic dynein light chain 1 (HDLC1)	U32944	-20	89
	3	99	beta-actin (ACTB)	K00790	336	375
	3	99	DNA helicase II, ATP-dependent, 70 kD subunit (KU70)	S38729	131	404
	47	~~143~~ 142	Beta-prime subunit of coatomer complex (COPP)	X70476	796	906
	3	99	Osteopontin, alt. transcript 1 (OSTP)	BC007016	1	56
	52	~~143~~ 142	Na^+/Ca^{2+}-exchange protein 1 (SLC8A1)	M91368	302	575
	52	~~143~~ 142	Catenin, alpha 2 (A2-CAT)	M94151	1	166
	52	~~143~~ 142	Catenin, alpha 2 (A2-CAT)	M94151	55	487